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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=11; hr=17; min=36; sec=25; ms=624; ]

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Application No: 10535522 Version No: 3.0

Input Set:

Output Set:

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Finished: 2009-05-05 16:25:51.056  
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 120 ms  
Total Warnings: 8  
Total Errors: 0  
No. of SeqIDs Defined: 13  
Actual SeqID Count: 13

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# SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding  
them for the Treatment or Prevention of Diseases

<130> 032723woJH

<140> 10535522

<141> 2006-04-13

<160> 13

<170> PatentIn Ver. 2.1

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<222> (1)..(615)

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gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac	96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp	
20 25 30	

ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc	144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser	
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tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag	192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln	
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gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt	240
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly	
65 70 75 80	

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac	288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn	
85 90 95	

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg	336
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro	
100 105 110	

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga	384
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly	

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tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag			432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu			
130	135	140	
att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att			480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			
145	150	155	160
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct			528
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser			
165	170	175	
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Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys			
180	185	190	
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Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser			
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Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln			
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Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn			
85	90	95	
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro			
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Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly			
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Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu			
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Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			

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Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys						
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gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct	97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala	
15 20 25	
tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag	145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln	
30 35 40	
ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag	193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu	
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Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro	
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Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser	
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Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn	
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ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct	385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala	
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aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc	433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe	
125 130 135 140	

tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt	481
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Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu	
160 165 170	
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Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val	
175 180 185	
acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggg ttttaciaaa	631
Thr Leu Pro Lys Thr Glu Thr Val	
190 195	
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taatgagctg ggctccttcc tcatttgctt cccaaagaga ttttgtccca ctaatgggtgt 1951

gcccattcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011

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 gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96  
 Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro  
 10 15 20  
  
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 Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu  
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 40 45 50 55  
  
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 75 80 85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336  
 Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu  
 90 95 100

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 Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys  
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Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly  
 40 45 50 55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn  
 60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser  
 75 80 85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu  
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Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn  
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Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser  
75 80 85  
  
ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336  
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu  
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Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys  
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sequence of pGEX2ThCD83ext\_mut129\_CtoS

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